

# Prediction of pork carcass composition based on cross-sectional region analysis of dual energy X-ray absorptiometry (DXA) scans<sup>☆</sup>

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Received 3 January 2002; received in revised form 15 March 2002; accepted 15 March 2002

## Abstract

Dual energy X-ray absorptiometry (DXA) was used to measure pork carcass composition by performing a total scan of the right half of 262 pork carcasses ( $42.7 \pm 5.2$  kg). The DXA scans were analyzed for percentage fat in the entire half-carcass as well as the shoulder, ham, loin, and side regions. In addition, a total of 14 cross-sections (57.6 mm wide) were analyzed: six in the shoulder/thoracic region, three in the loin region, and five in the ham region. Relative to the DXA measurement of total fat content, the coefficient of determination ( $R^2$ ) for a single cross-sectional slice ranged from 0.908 to 0.976. Relative to chemical analysis, a single slice from the ham region predicted the percentage of fat or lean in the half-carcass with an  $R^2$  of 0.81 and a standard error of the estimate of 2.04. Prediction equations were used to analyze a separate group of 65 half-carcasses. These results indicate that carcass fat and lean percentages can be measured by performing a single-pass cross-sectional scan that would be compatible with on-line processing. © 2002 Elsevier Science Ltd. All rights reserved.

**Keywords:** Carcass Composition; Dual energy X-ray absorptiometry; Pigs

## 1. Introduction

A rapid, accurate method is needed to provide information regarding the fat and lean content during the on-line processing of pork carcasses. The method should also be non-invasive and require little user input in terms of manipulation and data processing. Among the techniques that have been evaluated recently are: total body electrical conductivity (TOBEC; Berg, Engel & Forrest, 1998; Berg, Forrest, & Fisher, 1994); bioelectrical impedance (BIA; Swantek, Crenshaw, Marchello, & Lukaski, 1992; Swantek, Marchello, Tilton, & Crenshaw, 1999); ultrasound (Brøndum, Egebo, Agerskov, & Busk, 1998; Liu & Stauffer, 1995); and video image analysis (VIA; Branscheid & Dobrowolski, 1996; Branscheid, Dobrowolski, & Höreth, 1995; Stanford, Richmond, Jones, Robertson, Price, & Gordon, 1998). Other techniques may be

sufficiently accurate but have limitations that preclude serious consideration for on-line adaptation (Forrest, Kuei, Orcutt, Schinckel, Stouffer, & Judge, 1989).

Mainly, two techniques have been evaluated for automated on-line measurement of pork carcass composition. Using electromagnetic scanning or TOBEC in an on-line industrial configuration, Berg et al. (1994) reported the correlation ( $r$ ) of a variety of TOBEC readings with carcass measurements of total dissectible carcass lean (0.54–0.93), percentage of carcass lean (0.29–0.75), and total fat (–0.09–0.66). The same study reported prediction equations for total dissected carcass lean ( $R^2=0.83$ –0.90) and percentage of carcass lean ( $R^2=0.82$ –0.86). Ultrasound technology has been successfully adapted for on-line pork carcass evaluation. Liu and Stouffer (1995), using an ultrasound with a 3.5-MHz linear array transducer, reported an  $R^2$  of 0.88 for prediction of carcass lean weight. A fully automated system consisting of 16–2.0 MHz transducers described by Brøndum et al. (1998) predicted the meat percentage of pork carcasses with an accuracy (RSD) of 1.58–1.95%.

Dual energy X-ray absorptiometry (DXA) can be used to measure pork carcass composition by performing a total scan of the half-carcass (Mitchell, Scholz,

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Pursel, & Evock-Clover, 1998). The DXA scan can be analyzed for total or regional fat, lean, and bone mineral content, but is too slow for on-line slaughter application. DXA has also been used to measure the composition of beef rib sections (Mitchell, Solomon, & Rumsey, 1997) and de-boned meat samples (Brienne, Denoyelle, Baussart, & Daudin, 2001).

Studies have indicated that chemical analysis of cross-sections obtained at various locations throughout the carcass is highly correlated with total carcass fat (Doornenbal, 1972) and lean (Doornenbal, 1971). Similarly, Shields and Mahan (1983) reported a high correlation between the chemical analysis of sawdust obtained from cross-sectional cuts of the half-carcass and chemical analysis of the entire half-carcass. Also, the fat and muscle areas of cross-sectional images generated by magnetic resonance imaging (MRI) are highly correlated with the total body composition of pigs (Baulain, Henning, & Kallweit, 1996; Fowler, Fuller, Glasbey, Cameron, & Foster, 1992).

The purpose of the present study was to evaluate DXA scans of pork half-carcass to determine the feasibility of predicting carcass composition based on a single cross-sectional measurement.

## 2. Materials and methods

### 2.1. DXA scanning and analysis

A total of 262 pork half-carcasses (right side) were scanned by dual energy X-ray absorptiometry (DXA) using a GE Lunar (Madison, WI) DPX-L densitometer (adult-medium scan mode, software version 4.6d). This instrument utilized a pencil-beam X-ray technology, scanning at cross-sectional intervals of 9.6 mm with a scan speed of 7.68 cm/s. The collimation (size of the X-ray beam at the source) of the pencil-beam is 1.68 mm. The sample size is 4.8×9.6 mm. Thus, the sample interval (sampling time for each sample) was 0.0625 s. Each half-carcass was placed, skin side down (without hair removal), on the scan table and the entire half-carcass scanned anterior to posterior. Half-carcass weights ranged from 29.9 to 51.7 kg (mean=42.7±5.2 kg). The DXA automatically calculates and reports the amounts of total fat tissue, lean tissue (per DXA model definition: DXA lean=soft tissue–fat tissue), and bone mineral content. The amount of DXA fat and lean tissue is highly correlated ( $r>0.98$ ) to the measured soft tissue attenuation coefficient ( $R$ -value: ratio of attenuation coefficients at 38 and 70 keV). Attenuation is measured as the decrease in x-ray energy as it passes through the tissue relative to air. Calibration studies at DXA energies of 38 and 70 keV report that  $R$ -values range from 1.2 for fat to 1.4 for 100% lean. The technical principles of DXA have been described by Blake

and Fogelman (1997). A manual region-of-interest (ROI) analysis was performed for the shoulder, ham, loin and side (belly) regions as illustrated previously (Mitchell et al., 1998). The fat and lean tissue content was measured within each ROI. In addition, 14 cross-sectional regions (57.6 mm wide) were defined as illustrated in Fig. 1. Consecutive slices were constructed in the caudal direction, six in the shoulder/thoracic region, starting at the first rib (S 1–6); three in the loin region, starting at the last rib (L 1–3); and five in the ham region, starting at the anterior tip of the ache bone (H1–5). Each of these cross-sectional slices was analyzed as an individual ROI for fat and lean content.

### 2.2. Chemical analysis

After the carcasses had been scanned, they were ground and mixed in preparation for chemical analysis. Each half-carcass was ground using a whole-body grinder (Model 810, GH, Astoria, OR) fitted with a 0.32-cm sieve. The ground carcass was mixed by stirring and then passed through the grinder a second time. A 0.5-kg sample was used for protein and lipid analysis. Protein content of the carcass was measured on triplicate 2- to 3-g samples by the Kjeldahl procedure (Kjeldahl nitrogen: AOAC, 1984). Lipid analysis was performed on triplicate 5- to 7-g samples by the procedure of Folch, Lees, and Sloan-Stanley (1957). Water content of a duplicate 0.5-kg ground carcass sample was determined by lyophilization for 10 days. Chemical carcass “lean” was defined as the sum of protein and water.

### 2.3. Statistical analysis and prediction equations

Statistical analysis was performed using Statgraphics® Plus for Windows 2.1. Linear regression analysis was used to compare the DXA measurements of fat and lean percentages in the total carcass with those of the various regions and to compare DXA results with chemical analysis. Differences between means were evaluated by analysis of variance followed by a multiple range test (Fisher’s 95% LSD).

A separate group consisting of 65 half-carcasses weighing from 40.5 to 48.6 kg (44.8±1.8 kg) were scanned by DXA and then analyzed chemically as described above. These results were cross validated based on equations developed from the linear regression analysis of the first set of carcasses.

## 3. Results and discussion

### 3.1. DXA measurement of fat distribution

The DXA measurement for the distribution of the percentage of fat in the soft tissue of the various regions

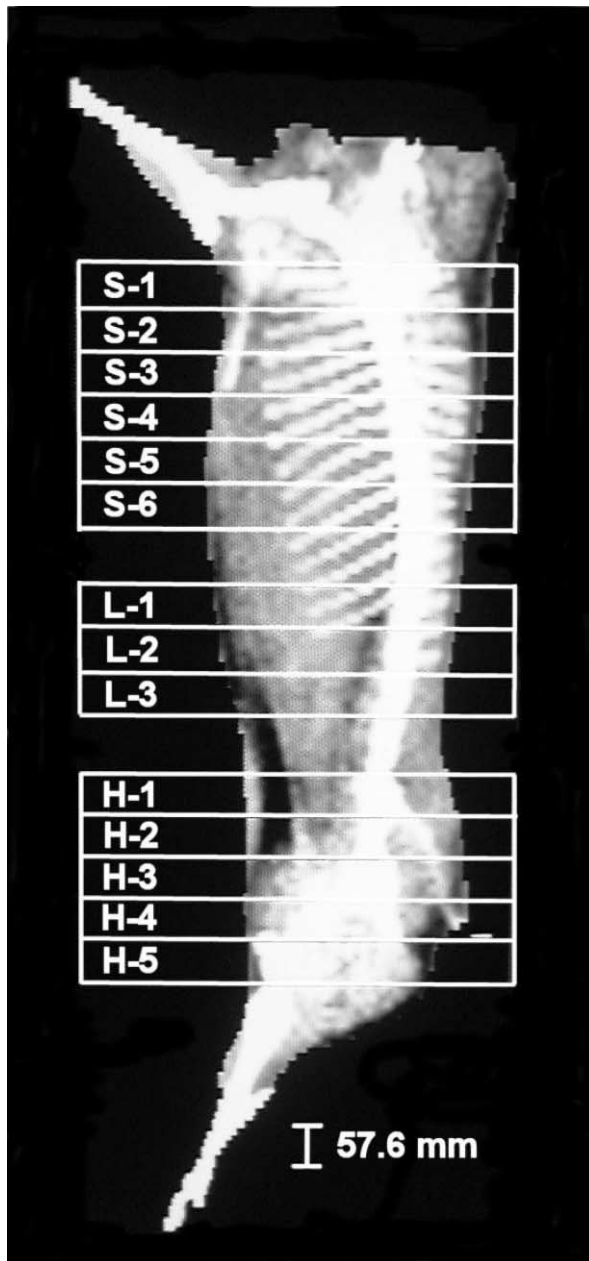


Fig. 1. Dual energy X-ray absorptiometry (DXA) scan of a pork half-carcass showing the cross-sectional slices that were evaluated for predicting carcass composition.

and cross-sectional slices of the half-carcass are shown in Table 1. The locations of the individual slices are shown in Fig. 1. Among the regions, the highest fat content was in the side. Among the slices, the highest fat content was in H1 and the lowest was in H3. The DXA measurement of the percentage of fat in the entire half-carcass was less ( $P < 0.05$ ) than that determined by chemical analysis. However, there was no difference in the fat content predicted from the DXA measurement using a previously reported prediction equation (Mitchell et al., 1998) and that determined by chemical analysis.

Table 1

Distribution of the dual energy X-ray absorptiometry (DXA) measurement of the percentage of fat in the soft tissue of the various regions and cross-sectional slices of the half carcass and DXA and chemical measurements of composition of the entire half-carcass

Region or slice <sup>a</sup>	Percentage fat <sup>b</sup>
<i>Region</i>	
Shoulder	23.69 ± 6.72cde
Ham	22.88 ± 6.74efg
Loin	23.63 ± 7.55cdef
Side	27.84 ± 7.58a
<i>Slices</i>	
S1	23.18 ± 7.72defg
S2	22.48 ± 7.02fg
S3	22.42 ± 6.75g
S4	22.79 ± 6.78efg
S5	24.43 ± 7.25bc
S6	24.54 ± 7.61bc
L1	25.36 ± 8.21b
L2	26.91 ± 8.50a
L3	26.89 ± 7.63a
H1	27.87 ± 6.84a
H2	22.03 ± 6.73g
H3	19.92 ± 6.39h
H4	22.56 ± 7.20efg
H5	22.43 ± 7.11fg
<i>Half-carcass</i>	
DXA	24.35 ± 7.25bcd
DXA, predicted <sup>c</sup>	27.98 ± 4.67a
Chemical analysis	27.76 ± 4.74a

<sup>a</sup> See Fig. 1 for locations.

<sup>b</sup> Means ± SD followed by different letters were different at  $P < 0.05$  (multiple range test).

<sup>c</sup> Fat (%) =  $450 - (315 \times \text{DXA } R \text{ value})$ ; Mitchell et al., 1998).

### 3.2. Relationship between fat measured by half-carcass DXA scan and fat measured in cross-sectional slices of DXA scan

In a previous study (Mitchell et al., 1998) using DXA to estimate the composition of pork carcasses, it was observed that the percentage of fat measured in a complete scan of the half-carcass correlated with the chemical analysis of fat with an  $r$  of 0.9 ( $R^2$  of 0.81). While a total carcass scan would be much too slow to be compatible with on-line processing, a single-pass scan rendering single slice information could be accomplished in less than 10 s. The rationale for this approach is based on the high relation between the composition of individual slices and total carcass composition. Doornenbal (1972) reported a close relationship between the area of fat in several cross-sections throughout the carcass and total carcass fat ( $R^2$  ranging from 0.94 to 0.98).

The DXA measurement of the percentage of fat in the soft tissue of each of the 14 individual slices was highly correlated ( $r = 0.953\text{--}0.988$ ;  $R^2 = 0.908\text{--}0.976$ ) with the DXA measurement of percentage of fat in the entire

half-carcass (Table 2). The highest relation ( $R^2$ ) was 0.976 for slices S5 and L1. The close relationship between the percentage of fat measured by DXA for the individual cross-sectional slices and the percentage of fat measured by DXA for the entire half-carcass is consistent with the results based on dissection and chemical analysis as reported by Doornenbal (1972).

### 3.3. Relationship between fat measured in regions of DXA scan and fat measured in cross-sectional slices of DXA scan

For the separate regions, the highest relationships between the fat content of an individual slice and the fat content of entire region were: shoulder, S1; loin, S5; side, L1; and ham, H3 and H4 (Table 2). Previously reported results (Mitchell et al., 1998) indicated that the composition of the primal cuts could be estimated by analyzing the shoulder, ham, loin, and side regions from a scan of the entire half-carcass. The results of this study (Table 2) further suggest that analysis of individual cross-sectional slices through these regions might also be used to predict composition of the primal cuts. Alternatively, the composition of different regions of the

Table 2

Regression analysis comparing dual energy X-ray absorptiometry (DXA) measurement of the percentage fat in the soft tissue of the half-carcass or specific region ( $Y$ ) to DXA measure of the percentage fat in the soft tissue of individual slices ( $X$ ) using the linear model  $Y = a + b \times X$

Half-carcass			Region		
Slice location	$R^2$	SEE <sup>a</sup>	Region/slice location	$R^2$	SEE <sup>a</sup>
<i>Shoulder</i>			<i>Shoulder</i>		
S1	0.969	1.371	S1	0.978	0.994
S2	0.965	1.320	S2	0.962	1.309
S3	0.957	1.415	S3	0.946	1.559
S4	0.950	1.519			
S5	0.976	1.126	<i>Loin</i>		
S6	0.975	1.211	S4	0.954	1.620
			S5	0.972	1.264
<i>Loin</i>			S6	0.963	1.459
L1	0.976	1.285	L1	0.965	1.425
L2	0.964	1.614	L2	0.949	1.704
L3	0.947	1.749	L3	0.919	2.152
<i>Ham</i>			<i>Side</i>		
H1	0.938	1.700	S6	0.948	1.740
H2	0.921	1.904	L1	0.960	1.520
H3	0.964	1.210	L2	0.956	1.592
H4	0.965	1.348	L3	0.942	1.831
H5	0.908	2.159	<i>Ham</i>		
			H1	0.942	1.635
			H2	0.942	1.622
			H3	0.972	1.125
			H4	0.972	1.122
			H5	0.919	1.928

<sup>a</sup> SEE = standard error of estimate.

carcass has been used to predict the composition of the entire carcass. The percentage of fat in the carcass is correlated with the percentage of lipid in the 3–6-rib section ( $R^2 = 0.42$ , Bacon, Loveday, Pace, & Riemann, 1989) and the percentage of fat in the ham and loin ( $R^2 = 0.61$  and  $0.47$ , respectively; Johnson, Miller, Haydon, & Reagan, 1990). The  $R^2$  values for the prediction of percentage of lipid in the carcass based on the DXA measured lipid content of the shoulder, loin, side, and ham (Table 3) are similar to those reported by Swensen, Ellis, Brewer, Novakofski, and McKeith (1998) based on the chemically determined lipid content of the same regions (0.82, 0.84, 0.80, and 0.72, respectively).

### 3.4. Relationship between chemical analysis of half-carcass and fat and lean measured in cross-sectional slices of DXA scan

The relationship between the DXA measurements of the percentage of fat in the soft tissue of cross-sectional slices and the chemical measurement of percentage of

Table 3

Regression analysis comparing chemical measurement of the percentage fat, protein or water in the half-carcass ( $Y$ ) to the dual energy X-ray absorptiometry (DXA) measure of the percentage fat (or lean for protein and water) in the soft tissue of individual slices or regions ( $X$ ) using the linear model  $Y = a + b \times X$

Slice or region location	Fat (%)		Protein (%)		Water (%)	
	$R^2$	SEE <sup>a</sup>	$R^2$	SEE	$R^2$	SEE
<i>Shoulder</i>						
S1	0.728	2.457	0.464	0.851	0.763	1.841
S2	0.766	2.279	0.456	0.857	0.796	1.711
S3	0.747	2.368	0.439	0.870	0.777	1.786
S4	0.763	2.295	0.456	0.857	0.777	1.786
S5	0.792	2.147	0.488	0.832	0.802	1.682
S6	0.779	2.215	0.474	0.843	0.798	1.701
<i>Loin</i>						
L1	0.784	2.188	0.484	0.835	0.810	1.651
L2	0.782	2.201	0.461	0.853	0.801	1.688
L3	0.788	2.167	0.482	0.837	0.811	1.644
<i>Ham</i>						
H1	0.799	2.112	0.526	0.800	0.841	1.510
H2	0.813	2.039	0.495	0.826	0.872	1.573
H3	0.800	2.105	0.505	0.818	0.831	1.558
H4	0.757	2.322	0.490	0.830	0.811	1.643
H5	0.747	2.369	0.475	0.842	0.803	1.678
<i>Region<sup>b</sup></i>						
Shoulder	0.775	2.233				
Loin	0.792	2.148				
Side	0.772	2.247				
Ham	0.790	2.161				

<sup>a</sup> SEE = standard error of estimate.

<sup>b</sup> DXA analysis by region; when the DXA scan of the half-carcass was partitioned into four separate regions rather than cross-sectional slices.

Table 4

Prediction equations for the estimation of percentage of fat and lean in the half-carcass using dual energy X-ray absorptiometry (DXA)

<i>Estimation of percentage fat in half-carcass</i>	
DXA scan of entire half-carcass	
FAT% = $13.5 + (0.582 \times \text{DXA FAT\%})$	( $R^2 = 0.81$ , SEE = 2.09)
FAT% = $422 - (295 \times \text{DXA R value})$	( $R^2 = 0.81$ , SEE = 2.03)
Single DXA cross-sectional slice	
FAT% = $13.7 + (0.62 \times \text{H2 FAT\%})$	( $R^2 = 0.81$ , SEE = 2.04)
Combination of three DXA slices	
FAT% = $13.1 + (0.338 \times \text{H2 FAT\%}) + (0.130 \times \text{S5 FAT\%}) + (0.136 \times \text{L3 FAT\%})$	( $R^2 = 0.82$ , SEE = 1.95)
<i>Estimation of percentage lean in half-carcass</i>	
DXA scan of entire half-carcass	
LEAN% = $25.2 + (0.584 \times \text{DXA LEAN\%})$	( $R^2 = 0.81$ , SEE = 2.07)
LEAN% = $-320 + (289 \times \text{DXA R value})$	( $R^2 = 0.82$ , SEE = 1.97)
Single DXA cross-sectional slice	
LEAN% = $20.6 + (0.61 \times \text{H2 LEAN\%})$	( $R^2 = 0.82$ , SEE = 2.00)
Combination of three DXA slices	
LEAN% = $22.9 + (0.352 \times \text{H2 LEAN\%}) + (0.0922 \times \text{S5 LEAN\%}) + (0.151 \times \text{L3 LEAN\%})$	( $R^2 = 0.83$ , SEE = 1.93)

fat in the entire half-carcass is shown in Table 3. The coefficients of determination ( $R^2$ ) ranged from 0.728 for S1 in the shoulder region to 0.813 for H2 from the ham region. The relationship between the fat measured by DXA for the cross-sectional slices and chemically determined percentage of fat in the half carcass are consistent with the overall relationship for the measurement of percentage of fat in the half-carcass based on the total scan (Mitchell et al., 1998).

Typically, the percentage of protein in the carcass is difficult to predict accurately. Although statistically significant ( $P < 0.001$ ), the relationship between the DXA measurement of the percentage of lean in the soft tissue of the cross-sectional slices and the chemical measurement of percentage of protein in the half-carcass was much lower than observed for fat content. The coefficient of determination ( $R^2$ ) between the percentage lean in DXA cross-sectional slices and the percentage protein in the half-carcass ranged from 0.439 for S3 in the shoulder region to 0.526 for H1 in the ham region (Table 3), compared to 0.29 calculated from the lean content of the 3–6 rib section in the study by Bacon et al. (1989). In the study by Doornenbal (1971) it was shown that the chemically measured protein content of cross-sectional slices made at various locations throughout the length of the pork carcass were highly correlated with the total amount of protein in the entire half-carcass ( $R^2 = 0.78$ – $0.95$ ). From the data of Shields and Mahan (1983) there was a correlation ( $R^2$ ) of 0.59 ( $r = 0.77$ ) between the amount of protein in the carcass and the amount of protein in the residue collected from sawing the carcass at 2.54-cm intervals in cross-section.

The relation between the DXA measurement of the percentage of lean in the soft tissue of the cross-sectional slices and the chemical measurement of per-

centage of water in the half-carcass was slightly higher than observed for fat content. The coefficients of determination ( $R^2$ ) ranged from 0.763 for S1 in the shoulder region to 0.872 for H2 in the ham region (Table 3). From the studies by Shields and Mahan (1983) and Bacon et al. (1989) the relationship between carcass water content and either the lean or water content of the sampled area is similar to the relationship between the fat content of the same components. Likewise, in the present study the relationship between the water content of the half-carcass and the lean content of the DXA cross-sectional slices was similar to the relationship between the fat content of the same components.

### 3.5. Prediction equations

Based on the relationships between chemical analysis of the half-carcasses and DXA results, equations were developed for predicting the percentages of fat or lean in the half-carcass using either the DXA information from the entire half-carcass, a single slice (H2), or a combination of three slices (H2, S5, and L3). These locations were chosen based on their high  $R^2$  with several parameters. These prediction equations are presented in Table 4. These equations were then used to predict the percentages of fat and lean in a separate group of 65 carcasses. By chemical analysis, the fat content of these carcasses ranged from 16.8 to 39.8% (average, 26.0%). The equation for the prediction of percentage of carcass fat based on the DXA R value (attenuation ratio) from the scan of the entire half-carcass differs slightly from the equation presented in an earlier study (Mitchell et al., 1998). Thus, it appears that the single DXA cross-sectional slice H2 from the ham region is as accurate as the information obtained from a scan of the entire half-carcass for predicting fat content. The inclusion of two additional slices, S5 from the shoulder region and L3 from the loin region, improved the prediction only very slightly. From the results of this study, prediction equations were developed for the estimation of percentage of lean in the half-carcass (Table 4). As was the case for the prediction of fat content, it appears that the single DXA cross-sectional slice H2 from the ham region is nearly as accurate as the information obtained from a scan of the entire half-carcass for predicting lean content. Likewise, the inclusion of two additional slices, S5 from the shoulder region and L3 from the loin region, only slightly improved the prediction of lean content. A comparison of the chemical measurements for percentages of fat and “lean” and the values predicted using a single slice (H2) are shown in Figs. 2 and 3. Within this group of half-carcass samples, 51% of the predicted fat values were within 5% of the regression line and 77% were within 10%. For the prediction of percentage of lean, 91% of the predicted lean values were within 5% of the regression line.

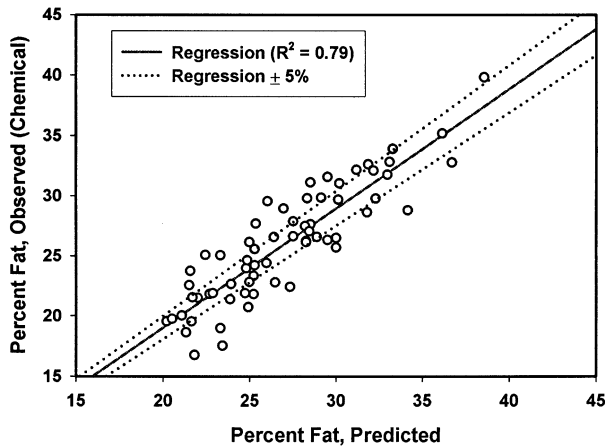


Fig. 2. Prediction of carcass fat content using a single slice (H2 FAT%) from a dual energy X-ray absorptiometry (DXA) scan of the half-carcass from a total of 65 pork carcasses.

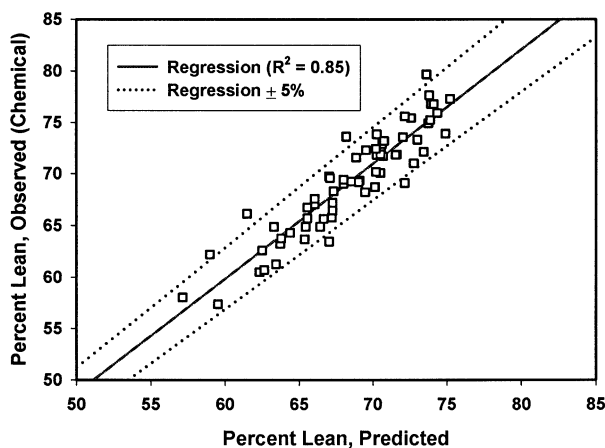


Fig. 3. Prediction of carcass lean content using a single slice (H2 LEAN%) from a dual energy X-ray absorptiometry (DXA) scan of the half-carcass from a total of 65 pork carcasses.

#### 4. Implications

In summary, the results of this study are consistent with those of other studies that indicate that the composition of a cross-section of the pork carcass is highly correlated with the composition of the entire carcass. In addition, this study demonstrates that the cross-sectional composition can be measured using dual energy X-ray absorptiometry. The implication is that this approach may be adaptable to on-line evaluation of pork carcasses.

The DXA instrument used in this study utilized the pencil-beam X-ray technology, scanning at cross-sectional intervals of 9.6 mm at a scan speed of 7.68 cm/s. Typically DXA instruments scan at rates of 4–16 cm/s. With these units the subject remains stationary and the scan speed is determined by the simultaneous motor-driven movement of the X-ray source and detector. Scan velocity has been shown to influence the

measurement of fat and lean mass (Black et al., 2002). By comparison, the chain speed of a modern slaughter facility is approximately 16.6 cm/s.

Newer DXA instruments utilize a wide-angle or fan-beam technology that will scan wider sections. For example the GE-Lunar Prodigy™ model utilizes the wide-angle technology to produce an effective beam width of 18.3 mm that is 56 mm wide by the time it reaches the detector and the Hologic QDR-4500™ utilizes the fan-beam technology to produce an effective beam width of 13 mm that is 260 mm when it reaches the detector(s). The effective beam width is width of the X-ray beam at 10 cm above the top of the scan table, while the detector is approximately 45 cm above the top of the scan table. Comparative studies indicate that the pencil and wide-angle beam are comparable for measuring soft tissue composition (Nord, Homuth, Hanson, & Mazess, 2000). Therefore, in the present study, 57.9 mm wide cross-sectional regions were analyzed (representing 6×9.6 mm scan lines) in order to approximate the information that might be obtained in a single slice using the wide-angle or fan-beam technology, which was not available for the present study.

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